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## **Reply to Hauser et al**

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### Reply to Hauser et al

TO THE EDITOR—We appreciate the letter by Hauser and colleagues [1] describing an outbreak of *Pneumocystis* pneumonia in Frankfurt [2]. The outbreak appears to be caused by the same strain of *Pneumocystis*, which we have called the European Renal Transplant (ERT) strain, that we

had previously shown was responsible for outbreaks in Munich and Zurich [3–5]. This observation reflects the importance of strain typing, but also highlights the need for well-conducted epidemiologic investigations to better understand the source and mode of *Pneumocystis* infection transmission in these populations.

It is now clear from multiple reports that outbreaks of *Pneumocystis* pneumonia can be caused by a single strain of the organism, and that close contact among susceptible individuals may be responsible for the transmission of the organism and maintenance of the outbreak (reviewed in [6]). The Lyon outbreak appeared to involve 1 of the most prevalent strains (based on typing by single-strand conformational polymorphism analysis) [7], and thus may have simply reflected exposure to that strain. However, the available data argue against that explanation in these 3 related outbreaks, when it is taken into account that none of the 11 isolates (6 from Munich, 3 from Zurich, and 2 from Frankfurt) obtained contemporaneously from non-outbreak patients were the ERT strain [1, 3].

Only 4 isolates were sequenced, and thus it is possible that other *Pneumocystis* strains were responsible for the additional 26 cases identified in the Frankfurt outbreak [2]. Nonetheless, it is striking that 3 outbreaks of PCP in 3 cities approximately 300 to 400 km apart were associated with a single strain of *Pneumocystis*. We agree that typing of additional contemporaneous isolates from endemic cases as well as from individuals with subclinical *Pneumocystis* infection would be needed to clarify the epidemiology. However, since these outbreaks occurred approximately 5–7 years ago, it would be very difficult to obtain such samples or retrospectively perform a detailed epidemiologic investigation to try to identify sources of infection that may have linked the outbreaks. Based on these observations, it is critical that future outbreaks be diligently investigated so that we may better understand the sources of infection and the mode of transmission, and to

determine if the ERT strain or other strains are associated with multiple outbreaks. We currently do not have the tools to readily identify and study virulence factors due to an inability to culture the organism and a lack of a genome sequence for *P. jirovecii*. However, once these tools become available, they need to be applied to better understand the biology of this infection. Until then, we feel that strain typing plays an important role in elucidating the transmission dynamics of *Pneumocystis* infection.

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